

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Chen, J. Don
Li, Hui

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(ii) TITLE OF INVENTION: Transcriptional Coactivator for Nuclear
Hormone Receptors

(iii) NUMBER OF SEQUENCES: 2

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lahive and Cockfield
(B) STREET: 28 State Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

30

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Liepmann, W. Hugo
(B) REGISTRATION NUMBER: 20,407
(C) REFERENCE/DOCKET NUMBER: UMM-026

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-227-7400
(B) TELEFAX: 617-742-4214

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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(A) NAME/KEY: CDS
(B) LOCATION: 86..4338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 GCTGGATGGT GGA CTCAGAG ACCAATAAAA ATAACTGCT TGAACATCCT TTGACTGGTT 60
AGCCAGTTGC TGATGTATAT TCAAG ATG AGT GGA TTA GGA GAA AAC TTG GAT 112
Met Ser Gly Leu Gly Glu Asn Leu Asp
1 5

10 CCA CTG GCC AGT GAT TCA CGA AAA CGC AAA TTG CCA TGT GAT ACT CCA 160
Pro Leu Ala Ser Asp Ser Arg Lys Arg Lys Leu Pro Cys Asp Thr Pro
10 15 20 25

15 GGA CAA GGT CTT ACC TGC AGT GGT GAA AAA CGG AGA CGG GAG CAG GAA 208
Gly Gln Gly Leu Thr Cys Ser Gly Glu Lys Arg Arg Arg Glu Gln Glu
30 35 40

20 AGT AAA TAT ATT GAA GAA TTG GCT GAG CTG ATA TCT GCC AAT CTT AGT 256
Ser Lys Tyr Ile Glu Glu Leu Ala Glu Leu Ile Ser Ala Asn Leu Ser
45 50 55

25 GAT ATT GAC AAT TTC AAT GTC AAA CCA GAT AAA TGT GCG ATT TTA AAG 304
Asp Ile Asp Asn Phe Asn Val Lys Pro Asp Lys Cys Ala Ile Leu Lys
60 65 70

30 GAA ACA GTA AGA CAG ATA CGT CAA ATA AAA GAG CAA GGA AAA ACT ATT 352
Glu Thr Val Arg Gln Ile Arg Gln Ile Lys Glu Gln Gly Lys Thr Ile
75 80 85

35 TCC AAT GAT GAT GAT GTT CAA AAA GCC GAT GTA TCT TCT ACA GGG CAG 400
Ser Asn Asp Asp Asp Val Gln Lys Ala Asp Val Ser Ser Thr Gly Gln
90 95 100 105

40 GGA GTT ATT GAT AAA GAC TCC TTA GGA CCG CTT TTA CTT CAG GCA TTG 448
Gly Val Ile Asp Lys Asp Ser Leu Gly Pro Leu Leu Leu Gln Ala Leu
110 115 120

45 GAT GGT TTC CTA TTT GTG GTG AAT CGA GAG GCA AAC ATT GTA TTT GTA 496
Asp Gly Phe Leu Phe Val Val Asn Arg Glu Ala Asn Ile Val Phe Val
125 130 135

50 TCA GAA AAT GTC ACA CAA TAC CTG CAA TAT AAG CAA GAG GAC CTG GTT 544
Ser Glu Asn Val Thr Gln Tyr Leu Gln Tyr Lys Gln Glu Asp Leu Val
140 145 150

55 AAC ACA AGT GTT TAC AAT ATC TTA CAT GAA GAA GAC AGA AAG GAT TTT 592
Asn Thr Ser Val Tyr Asn Ile Leu His Glu Glu Asp Arg Lys Asp Phe
155 160 165

60 CTT AAG AAT TTA CCA AAA TCT ACA GTT AAT GGA GTT TCC TGG ACA AAT 640
Leu Lys Asn Leu Pro Lys Ser Thr Val Asn Gly Val Ser Trp Thr Asn
170 175 180 185

65 GAG ACC CAA AGA CAA AAA AGC CAT ACA TTT AAT TGC CGT ATG TTG ATG 688
Glu Thr Gln Arg Gln Lys Ser His Thr Phe Asn Cys Arg Met Leu Met
190 195 200

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	AAA	ACA	CCA	CAT	GAT	ATT	CTG	GAA	GAC	ATA	AAC	GCC	AGT	CCT	GAA	ATG	736
	Lys	Thr	Pro	His	Asp	Ile	Leu	Glu	Asp	Ile	Asn	Ala	Ser	Pro	Glu	Met	
				205					210					215			
5	CGC	CAG	AGA	TAT	GAA	ACA	ATG	CAG	TGC	TTT	GCC	CTG	TCT	CAG	CCA	CGA	784
	Arg	Gln	Arg	Tyr	Glu	Thr	Met	Gln	Cys	Phe	Ala	Leu	Ser	Gln	Pro	Arg	
			220					225					230				
10	GCT	ATG	ATG	GAG	GAA	GGG	GAA	GAT	TTG	CAA	TCT	TGT	ATG	ATC	TGT	GTG	832
	Ala	Met	Met	Glu	Glu	Gly	Glu	Asp	Leu	Gln	Ser	Cys	Met	Ile	Cys	Val	
		235					240					245					
15	GCA	CGC	CGC	ATT	ACT	ACA	GGA	GAA	AGA	ACA	TTT	CCA	TCA	AAC	CCT	GAG	880
	Ala	Arg	Arg	Ile	Thr	Thr	Gly	Glu	Arg	Thr	Phe	Pro	Ser	Asn	Pro	Glu	
	250					255					260					265	
20	AGC	TTT	ATT	ACC	AGA	CAT	GAT	CTT	TCA	GGA	AAG	GTT	GTC	AAT	ATA	GAT	928
	Ser	Phe	Ile	Thr	Arg	His	Asp	Leu	Ser	Gly	Lys	Val	Val	Asn	Ile	Asp	
					270					275					280		
25	ACA	AAT	TCA	CTG	AGA	TCC	TCC	ATG	AGG	CCT	GGC	TTT	GAA	GAT	ATA	ATC	976
	Thr	Asn	Ser	Leu	Arg	Ser	Ser	Met	Arg	Pro	Gly	Phe	Glu	Asp	Ile	Ile	
				285					290					295			
30	CGA	AGG	TGT	ATT	CAG	AGA	TTT	TTT	AGT	CTA	AAT	GAT	GGG	CAG	TCA	TGG	1024
	Arg	Arg	Cys	Ile	Gln	Arg	Phe	Phe	Ser	Leu	Asn	Asp	Gly	Gln	Ser	Trp	
			300					305					310				
35	TCC	CAG	AAA	CGT	CAC	TAT	CAA	GAA	GCT	TAT	CTT	AAT	GGC	CAT	GCA	GAA	1072
	Ser	Gln	Lys	Arg	His	Tyr	Gln	Glu	Ala	Tyr	Leu	Asn	Gly	His	Ala	Glu	
		315					320					325					
40	ACC	CCA	GTA	TAT	CGA	TTC	TCG	TTG	GCT	GAT	GGA	ACT	ATA	GTG	ACT	GCA	1120
	Thr	Pro	Val	Tyr	Arg	Phe	Ser	Leu	Ala	Asp	Gly	Thr	Ile	Val	Thr	Ala	
	330					335					340					345	
45	CAG	ACA	AAA	AGC	AAA	CTC	TTC	CGA	AAT	CCT	GTA	ACA	AAT	GAT	CGA	CAT	1168
	Gln	Thr	Lys	Ser	Lys	Leu	Phe	Arg	Asn	Pro	Val	Thr	Asn	Asp	Arg	His	
					350					355					360		
50	GGC	TTT	GTC	TCA	ACC	CAC	TTC	CTT	CAG	AGA	GAA	CAG	AAT	GGA	TAT	AGA	1216
	Gly	Phe	Val	Ser	Thr	His	Phe	Leu	Gln	Arg	Glu	Gln	Asn	Gly	Tyr	Arg	
				365					370					375			
55	CCA	AAC	CCA	AAT	CCT	GTT	GGA	CAA	GGG	ATT	AGA	CCA	CCT	ATG	GCT	GGA	1264
	Pro	Asn	Pro	Asn	Pro	Val	Gly	Gln	Gly	Ile	Arg	Pro	Pro	Met	Ala	Gly	
			380					385					390				
60	TGC	AAC	AGT	TCG	GTA	GGC	GGC	ATG	AGT	ATG	TCG	CCA	AAC	CAA	GGC	TTA	1312
	Cys	Asn	Ser	Ser	Val	Gly	Gly	Met	Ser	Met	Ser	Pro	Asn	Gln	Gly	Leu	
		395					400					405					
65	CAG	ATG	CCG	AGC	AGC	AGG	GCC	TAT	GGC	TTG	GCA	GAC	CCT	AGC	ACC	ACA	1360
	Gln	Met	Pro	Ser	Ser	Arg	Ala	Tyr	Gly	Leu	Ala	Asp	Pro	Ser	Thr	Thr	
	410					415					420					425	
70	GGG	CAG	ATG	AGT	GGA	GCT	AGG	TAT	GGG	GGT	TCC	AGT	AAC	ATA	GCT	TCA	1408

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	Gly	Gln	Met	Ser	Gly	Ala	Arg	Tyr	Gly	Gly	Ser	Ser	Asn	Ile	Ala	Ser	
					430					435					440		
5	TTG	ACC	CCT	GGG	CCA	GGC	ATG	CAA	TCA	CCA	TCT	TCC	TAC	CAG	AAC	AAC	1456
	Leu	Thr	Pro	Gly	Pro	Gly	Met	Gln	Ser	Pro	Ser	Ser	Tyr	Gln	Asn	Asn	
				445					450					455			
10	AAC	TAT	GGG	CTC	AAC	ATG	AGT	AGC	CCC	CCA	CAT	GGG	AGT	CCT	GGT	CTT	1504
	Asn	Tyr	Gly	Leu	Asn	Met	Ser	Ser	Pro	Pro	His	Gly	Ser	Pro	Gly	Leu	
			460					465					470				
15	GCC	CCA	AAC	CAG	CAG	AAT	ATC	ATG	ATT	TCT	CCT	CGT	AAT	CGT	GGG	AGT	1552
	Ala	Pro	Asn	Gln	Gln	Asn	Ile	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	Ser	
		475					480					485					
20	CCA	AAG	ATA	GCC	TCA	CAT	CAG	TTT	TCT	CCT	GTT	GCA	GGT	GTG	CAC	TCT	1600
	Pro	Lys	Ile	Ala	Ser	His	Gln	Phe	Ser	Pro	Val	Ala	Gly	Val	His	Ser	
	490					495					500					505	
25	CCC	ATG	GCA	TCT	TCT	GGC	AAT	ACT	GGG	AAC	CAC	AGC	TTT	TCC	AGC	AGC	1648
	Pro	Met	Ala	Ser	Ser	Gly	Asn	Thr	Gly	Asn	His	Ser	Phe	Ser	Ser	Ser	
					510					515					520		
30	TCT	CTC	AGT	GCC	CTG	CAA	GCC	ATC	AGT	GAA	GGT	GTG	GGG	ACT	TCC	CTT	1696
	Ser	Leu	Ser	Ala	Leu	Gln	Ala	Ile	Ser	Glu	Gly	Val	Gly	Thr	Ser	Leu	
				525					530					535			
35	TTA	TCT	ACT	CTG	TCA	TCA	CCA	GGC	CCC	AAA	TTG	GAT	AAC	TCT	CCC	AAT	1744
	Leu	Ser	Thr	Leu	Ser	Ser	Pro	Gly	Pro	Lys	Leu	Asp	Asn	Ser	Pro	Asn	
			540					545					550				
40	ATG	AAT	ATT	ACC	CAA	CCA	AGT	AAA	GTA	AGC	AAT	CAG	GAT	TCC	AAG	AGT	1792
	Met	Asn	Ile	Thr	Gln	Pro	Ser	Lys	Val	Ser	Asn	Gln	Asp	Ser	Lys	Ser	
		555					560					565					
45	CCT	CTG	GGC	TTT	TAT	TGC	GAC	CAA	AAT	CCA	GTG	GAG	AGT	TCA	ATG	TGT	1840
	Pro	Leu	Gly	Phe	Tyr	Cys	Asp	Gln	Asn	Pro	Val	Glu	Ser	Ser	Met	Cys	
	570					575					580					585	
50	CAG	TCA	AAT	AGC	AGA	GAT	CAC	CTC	AGT	GAC	AAA	GAA	AGT	AAG	GAG	AGC	1888
	Gln	Ser	Asn	Ser	Arg	Asp	His	Leu	Ser	Asp	Lys	Glu	Ser	Lys	Glu	Ser	
					590					595					600		
55	AGT	GTT	GAG	GGG	GCA	GAG	AAT	CAA	AGG	GGT	CCT	TTG	GAA	AGC	AAA	GGT	1936
	Ser	Val	Glu	Gly	Ala	Glu	Asn	Gln	Arg	Gly	Pro	Leu	Glu	Ser	Lys	Gly	
				605					610					615			
60	CAT	AAA	AAA	TTA	CTG	CAG	TTA	CTT	ACC	TGT	TCT	TCT	GAT	GAC	CGG	GGT	1984
	His	Lys	Lys	Leu	Leu	Gln	Leu	Leu	Thr	Cys	Ser	Ser	Asp	Asp	Arg	Gly	
			620					625					630				
65	CAT	TCC	TCC	TTG	ACC	AAC	TCC	CCC	CTA	GAT	TCA	AGT	TGT	AAA	GAA	TCT	2032
	His	Ser	Ser	Leu	Thr	Asn	Ser	Pro	Leu	Asp	Ser	Ser	Cys	Lys	Glu	Ser	
		635					640					645					
70	TCT	GTT	AGT	GTC	ACC	AGC	CCC	TCT	GGA	GTC	TCC	TCC	TCT	ACA	TCT	GGA	2080
	Ser	Val	Ser	Val	Thr	Ser	Pro	Ser	Gly	Val	Ser	Ser	Ser	Thr	Ser	Gly	

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	650				655					660				665			
	GGA	GTA	TCC	TCT	ACA	TCC	AAT	ATG	CAT	GGG	TCA	CTG	TTA	CAA	GAG	AAG	2128
5	Gly	Val	Ser	Ser	Thr	Ser	Asn	Met	His	Gly	Ser	Leu	Leu	Gln	Glu	Lys	
					670					675					680		
	CAC	CGG	ATT	TTG	CAC	AAG	TTG	CTG	CAG	AAT	GGG	AAT	TCA	CCA	GCT	GAG	2176
	His	Arg	Ile	Leu	His	Lys	Leu	Leu	Gln	Asn	Gly	Asn	Ser	Pro	Ala	Glu	
10				685					690					695			
	GTA	GCC	AAG	ATT	ACT	GCA	CAA	GCC	ACT	GGG	AAA	GAC	ACC	AGC	AGT	ATA	2224
	Val	Ala	Lys	Ile	Thr	Ala	Gln	Ala	Thr	Gly	Lys	Asp	Thr	Ser	Ser	Ile	
			700					705					710				
15	ACT	TCT	TGT	GGG	GAC	GGA	AAT	GTT	GTC	AAG	CAG	GAG	CAG	CTA	AGT	CCT	2272
	Thr	Ser	Cys	Gly	Asp	Gly	Asn	Val	Val	Lys	Gln	Glu	Gln	Leu	Ser	Pro	
		715					720					725					
20	AAG	AAG	AAG	GAG	AAT	AAT	GCA	CTT	CTT	AGA	TAC	CTG	CTG	GAC	AGG	GAT	2320
	Lys	Lys	Lys	Glu	Asn	Asn	Ala	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Arg	Asp	
		730					735				740				745		
	GAT	CCT	AGT	GAT	GCA	CTC	TCT	AAA	GAA	CTA	CAG	CCC	CAA	GTG	GAA	GGA	2368
25	Asp	Pro	Ser	Asp	Ala	Leu	Ser	Lys	Glu	Leu	Gln	Pro	Gln	Val	Glu	Gly	
					750					755					760		
	GTG	GAC	AAT	AAA	ATG	AGT	CAG	TGC	ACC	AGC	TCC	ACC	ATT	CCT	AGC	TCA	2416
	Val	Asp	Asn	Lys	Met	Ser	Gln	Cys	Thr	Ser	Ser	Thr	Ile	Pro	Ser	Ser	
30				765				770						775			
	AGT	CAA	GAG	AAA	GAC	CCT	AAA	ATT	AAG	ACA	GAG	ACA	AGT	GAA	GAG	GGA	2464
	Ser	Gln	Glu	Lys	Asp	Pro	Lys	Ile	Lys	Thr	Glu	Thr	Ser	Glu	Glu	Gly	
			780					785					790				
35	TCT	GGA	GAC	TTG	GAT	AAT	CTA	GAT	GCT	ATT	CTT	GGT	GAT	CTG	ACT	AGT	2512
	Ser	Gly	Asp	Leu	Asp	Asn	Leu	Asp	Ala	Ile	Leu	Gly	Asp	Leu	Thr	Ser	
		795					800					805					
40	TCT	GAC	TTT	TAC	AAT	AAT	TCC	ATA	TCC	TCA	AAT	GGT	AGT	CAT	CTG	GGG	2560
	Ser	Asp	Phe	Tyr	Asn	Asn	Ser	Ile	Ser	Ser	Asn	Gly	Ser	His	Leu	Gly	
		810					815				820				825		
	ACT	AAG	CAA	CAG	GTG	TTT	CAA	GGA	ACT	AAT	TCT	CTG	GGT	TTG	AAA	AGT	2608
45	Thr	Lys	Gln	Gln	Val	Phe	Gln	Gly	Thr	Asn	Ser	Leu	Gly	Leu	Lys	Ser	
					830					835				840			
	TCA	CAG	TCT	GTG	CAG	TCT	ATT	CGT	CCT	CCA	TAT	AAC	CGA	GCA	GTG	TCT	2656
	Ser	Gln	Ser	Val	Gln	Ser	Ile	Arg	Pro	Pro	Tyr	Asn	Arg	Ala	Val	Ser	
				845					850					855			
50	CTG	GAT	AGC	CCT	GTT	TCT	GTT	GGC	TCA	AGT	CCT	CCA	GTA	AAA	AAT	ATC	2704
	Leu	Asp	Ser	Pro	Val	Ser	Val	Gly	Ser	Ser	Pro	Pro	Val	Lys	Asn	Ile	
			860					865					870				
55	AGT	GCT	TTC	CCC	ATG	TTA	CCA	AAG	CAA	CCC	ATG	TTG	GGT	GGG	AAT	CCA	2752
	Ser	Ala	Phe	Pro	Met	Leu	Pro	Lys	Gln	Pro	Met	Leu	Gly	Gly	Asn	Pro	
		875					880					885					

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5	AGA ATG ATG GAT AGT CAG GAA AAT TAT GGC TCA AGT ATG GGT GGG CCA Arg Met Met Asp Ser Gln Glu Asn Tyr Gly Ser Ser Met Gly Gly Pro 890 895 900 905	2800
10	AAC CGA AAT GTG ACT GTG ACT CAG ACT CCT TCC TCA GGA GAC TGG GGC Asn Arg Asn Val Thr Val Thr Gln Thr Pro Ser Ser Gly Asp Trp Gly 910 915 920	2848
15	TTA CCA AAC TCA AAG GCC GGC AGA ATG GAA CCT ATG AAT TCA AAC TCC Leu Pro Asn Ser Lys Ala Gly Arg Met Glu Pro Met Asn Ser Asn Ser 925 930 935	2896
20	ATG GGA AGA CCA GGA GGA GAT TAT AAT ACT TCT TTA CCC AGA CCT GCA Met Gly Arg Pro Gly Gly Asp Tyr Asn Thr Ser Leu Pro Arg Pro Ala 940 945 950	2944
25	CTG GGT GGC TCT ATT CCC ACA TTG CCT CTT CGG TCT AAT AGC ATA CCA Leu Gly Gly Ser Ile Pro Thr Leu Pro Leu Arg Ser Asn Ser Ile Pro 955 960 965	2992
30	GGT GCG AGA CCA GTA TTG CAA CAG CAG CAG CAG ATG CTT CAA ATG AGG Gly Ala Arg Pro Val Leu Gln Gln Gln Gln Met Leu Gln Met Arg 970 975 980 985	3040
35	CCT GGT GAA ATC CCC ATG GGA ATG GGG GCT AAT CCC TAT GGC CAA GCA Pro Gly Glu Ile Pro Met Gly Met Gly Ala Asn Pro Tyr Gly Gln Ala 990 995 1000	3088
40	GCA GCA TCT AAC CAA CTG GGT TCC TGG CCC GAT GGC ATG TTG TCC ATG Ala Ala Ser Asn Gln Leu Gly Ser Trp Pro Asp Gly Met Leu Ser Met 1005 1010 1015	3136
45	GAA CAA GTT TCT CAT GGC ACT CAA AAT AGG CCT CTT CTT AGG AAT TCC Glu Gln Val Ser His Gly Thr Gln Asn Arg Pro Leu Leu Arg Asn Ser 1020 1025 1030	3184
50	CTG GAT GAT CTT GTT GGG CCA CCT TCC AAC CTG GAA GGC CAG AGT GAC Leu Asp Asp Leu Val Gly Pro Pro Ser Asn Leu Glu Gly Gln Ser Asp 1035 1040 1045	3232
55	GAA AGA GCA TTA TTG GAC CAG CTG CAC ACT CTT CTC AGC AAC ACA GAT Glu Arg Ala Leu Leu Asp Gln Leu His Thr Leu Leu Ser Asn Thr Asp 1050 1055 1060 1065	3280
60	GCG ACA GGC CTG GAA GAA ATT GAC AGA GCT TTG GGC ATT CCT GAA CTT Ala Thr Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu 1070 1075 1080	3328
65	GTC AAT CAG GGA CAG GCA TTA GAG CCC AAA CAG GAT GCT TTC CAA GGC Val Asn Gln Gly Gln Ala Leu Glu Pro Lys Gln Asp Ala Phe Gln Gly 1085 1090 1095	3376
70	CAA GAA GCA GCA GTA ATG ATG GAT CAG AAG GCA GGA TTA TAT GGA CAG Gln Glu Ala Ala Val Met Met Asp Gln Lys Ala Gly Leu Tyr Gly Gln 1100 1105 1110	3424

	ACA	TAC	CCA	GCA	CAG	GGG	CCT	CCA	ATG	CAA	GGA	GGC	TTT	CAT	CTT	CAG	3472
	Thr	Tyr	Pro	Ala	Gln	Gly	Pro	Pro	Met	Gln	Gly	Gly	Phe	His	Leu	Gln	
		1115					1120					1125					
5	GGA	CAA	TCA	CCA	TCT	TTT	AAC	TCT	ATG	ATG	AAT	CAG	ATG	AAC	CAG	CAA	3520
	Gly	Gln	Ser	Pro	Ser	Phe	Asn	Ser	Met	Met	Asn	Gln	Met	Asn	Gln	Gln	
	1130					1135					1140					1145	
10	GGC	AAT	TTT	CCT	CTC	CAA	GGA	ATG	CAC	CCA	CGA	GCC	AAC	ATC	ATG	AGA	3568
	Gly	Asn	Phe	Pro	Leu	Gln	Gly	Met	His	Pro	Arg	Ala	Asn	Ile	Met	Arg	
					1150					1155					1160		
15	CCC	CGG	ACA	AAC	ACC	CCC	AAG	CAA	CTT	AGA	ATG	CAG	CTT	CAG	CAG	AGG	3616
	Pro	Arg	Thr	Asn	Thr	Pro	Lys	Gln	Leu	Arg	Met	Gln	Leu	Gln	Gln	Arg	
				1165				1170						1175			
20	CTG	CAG	GGC	CAG	CAG	TTT	TTG	AAT	CAG	AGC	CGA	CAG	GCA	CTT	GAA	TTG	3664
	Leu	Gln	Gly	Gln	Gln	Phe	Leu	Asn	Gln	Ser	Arg	Gln	Ala	Leu	Glu	Leu	
			1180				1185						1190				
25	AAA	ATG	GAA	AAC	CCT	ACT	GCT	GGT	GGT	GCT	GCG	GTG	ATG	AGG	CCT	ATG	3712
	Lys	Met	Glu	Asn	Pro	Thr	Ala	Gly	Gly	Ala	Ala	Val	Met	Arg	Pro	Met	
		1195					1200					1205					
30	ATG	CAG	CCC	CAG	CAG	GGT	TTT	CTT	AAT	GCT	CAA	ATG	GTC	GCC	CAA	CGC	3760
	Met	Gln	Pro	Gln	Gln	Gly	Phe	Leu	Asn	Ala	Gln	Met	Val	Ala	Gln	Arg	
	1210					1215					1220					1225	
35	AGC	AGA	GAG	CTG	CTA	AGT	CAT	CAC	TTC	CGA	CAA	CAG	AGG	GTG	GCT	ATG	3808
	Ser	Arg	Glu	Leu	Leu	Ser	His	His	Phe	Arg	Gln	Gln	Arg	Val	Ala	Met	
				1230						1235					1240		
40	ATG	ATG	CAG	CAG	CAG	CAA	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAA	3856
	Met	Met	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
				1245				1250						1255			
45	CAG	CAA	CAG	CAA	CAG	CAG	CAA	CAG	CAG	CAA	ACC	CAG	GCC	TTC	AGC	CCA	3904
	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Thr	Gln	Ala	Phe	Ser	Pro	
			1260					1265					1270				
50	CCT	CCT	AAT	GTG	ACT	GCT	TCC	CCC	AGC	ATG	GAT	GGG	CTT	TTG	GCA	GGA	3952
	Pro	Pro	Asn	Val	Thr	Ala	Ser	Pro	Ser	Met	Asp	Gly	Leu	Leu	Ala	Gly	
		1275					1280					1285					
55	CCC	ACA	ATG	CCA	CAA	GCT	CCT	CCG	CAA	CAG	TTT	CCA	TAT	CAA	CCA	AAT	4000
	Pro	Thr	Met	Pro	Gln	Ala	Pro	Pro	Gln	Gln	Phe	Pro	Tyr	Gln	Pro	Asn	
	1290					1295					1300					1305	
60	TAT	GGA	ATG	GGA	CAA	CAA	CCA	GAT	CCA	GCC	TTT	GGT	CGA	GTG	TCT	AGT	4048

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SECRETED

Met Met Gln His Pro Gln Ala Ala Ser Ile Tyr Gln Ser Ser Glu Met
1340 1345 1350

5 AAG GGC TGG CCA TCA GGA AAT TTG GCC AGG AAC AGC TCC TTT TCC CAG 4192
Lys Gly Trp Pro Ser Gly Asn Leu Ala Arg Asn Ser Ser Phe Ser Gln
1355 1360 1365

10 CAG CAG TTT GCC CAC CAG GGG AAT CCT GCA GTG TAT AGT ATG GTG CAC 4240
Gln Gln Phe Ala His Gln Gly Asn Pro Ala Val Tyr Ser Met Val His
1370 1375 1380 1385

15 ATG AAT GGC AGC AGT GGT CAC ATG GGA CAG ATG AAC ATG AAC CCC ATG 4288
Met Asn Gly Ser Ser Gly His Met Gly Gln Met Asn Met Asn Pro Met
1390 1395 1400

CCC ATG TCT GGC ATG CCT ATG GGT CCT GAT CAG AAA TAC TGC TGA CAT CT 4338
Pro Met Ser Gly Met Pro Met Gly Pro Asp Gln Lys Tyr Cys *
1405 1410 1415

20 CTGCACCAGG ACCTCTTAAG GAAACCACTG TACAAATGAC ACTGCACTAG GATTATTGGG 4398

AAGGAATCAT TGTTCCAGGC ATCCATCTTG GAAGAAAGGA CCAGCTTTGA GCTCCATCAA 4458

25 GGGTATTTTA AGTGATGTCA TTTGAGCAGG AATTCTAG 4496

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1417 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Gly Leu Gly Glu Asn Leu Asp Pro Leu Ala Ser Asp Ser Arg
1 5 10 15

40 Lys Arg Lys Leu Pro Cys Asp Thr Pro Gly Gln Gly Leu Thr Cys Ser
20 25 30

45 Gly Glu Lys Arg Arg Arg Glu Gln Glu Ser Lys Tyr Ile Glu Glu Leu
35 40 45

Ala Glu Leu Ile Ser Ala Asn Leu Ser Asp Ile Asp Asn Phe Asn Val
50 55 60

50 Lys Pro Asp Lys Cys Ala Ile Leu Lys Glu Thr Val Arg Gln Ile Arg
65 70 75 80

Gln Ile Lys Glu Gln Gly Lys Thr Ile Ser Asn Asp Asp Asp Val Gln
85 90 95

55 Lys Ala Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ser
100 105 110

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B6E1E0-466F4050

	Leu	Gly	Pro	Leu	Leu	Leu	Gln	Ala	Leu	Asp	Gly	Phe	Leu	Phe	Val	Val
			115					120					125			
5	Asn	Arg	Glu	Ala	Asn	Ile	Val	Phe	Val	Ser	Glu	Asn	Val	Thr	Gln	Tyr
	130						135					140				
	Leu	Gln	Tyr	Lys	Gln	Glu	Asp	Leu	Val	Asn	Thr	Ser	Val	Tyr	Asn	Ile
	145					150					155				160	
10	Leu	His	Glu	Glu	Asp	Arg	Lys	Asp	Phe	Leu	Lys	Asn	Leu	Pro	Lys	Ser
					165					170					175	
	Thr	Val	Asn	Gly	Val	Ser	Trp	Thr	Asn	Glu	Thr	Gln	Arg	Gln	Lys	Ser
15				180					185					190		
	His	Thr	Phe	Asn	Cys	Arg	Met	Leu	Met	Lys	Thr	Pro	His	Asp	Ile	Leu
			195					200					205			
20	Glu	Asp	Ile	Asn	Ala	Ser	Pro	Glu	Met	Arg	Gln	Arg	Tyr	Glu	Thr	Met
	210						215					220				
	Gln	Cys	Phe	Ala	Leu	Ser	Gln	Pro	Arg	Ala	Met	Met	Glu	Glu	Gly	Glu
25	225					230					235				240	
	Asp	Leu	Gln	Ser	Cys	Met	Ile	Cys	Val	Ala	Arg	Arg	Ile	Thr	Thr	Gly
					245					250					255	
	Glu	Arg	Thr	Phe	Pro	Ser	Asn	Pro	Glu	Ser	Phe	Ile	Thr	Arg	His	Asp
30				260					265					270		
	Leu	Ser	Gly	Lys	Val	Val	Asn	Ile	Asp	Thr	Asn	Ser	Leu	Arg	Ser	Ser
			275				280						285			
35	Met	Arg	Pro	Gly	Phe	Glu	Asp	Ile	Ile	Arg	Arg	Cys	Ile	Gln	Arg	Phe
	290						295					300				
	Phe	Ser	Leu	Asn	Asp	Gly	Gln	Ser	Trp	Ser	Gln	Lys	Arg	His	Tyr	Gln
	305					310					315				320	
40	Glu	Ala	Tyr	Leu	Asn	Gly	His	Ala	Glu	Thr	Pro	Val	Tyr	Arg	Phe	Ser
					325					330					335	
	Leu	Ala	Asp	Gly	Thr	Ile	Val	Thr	Ala	Gln	Thr	Lys	Ser	Lys	Leu	Phe
45				340					345					350		
	Arg	Asn	Pro	Val	Thr	Asn	Asp	Arg	His	Gly	Phe	Val	Ser	Thr	His	Phe
			355					360					365			
50	Leu	Gln	Arg	Glu	Gln	Asn	Gly	Tyr	Arg	Pro	Asn	Pro	Asn	Pro	Val	Gly
	370						375					380				
	Gln	Gly	Ile	Arg	Pro	Pro	Met	Ala	Gly	Cys	Asn	Ser	Ser	Val	Gly	Gly
	385					390					395				400	
55	Met	Ser	Met	Ser	Pro	Asn	Gln	Gly	Leu	Gln	Met	Pro	Ser	Ser	Arg	Ala
					405					410					415	

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	Tyr	Gly	Leu	Ala	Asp	Pro	Ser	Thr	Thr	Gly	Gln	Met	Ser	Gly	Ala	Arg
				420					425					430		
5	Tyr	Gly	Gly	Ser	Ser	Asn	Ile	Ala	Ser	Leu	Thr	Pro	Gly	Pro	Gly	Met
			435					440					445			
	Gln	Ser	Pro	Ser	Ser	Tyr	Gln	Asn	Asn	Asn	Tyr	Gly	Leu	Asn	Met	Ser
		450					455					460				
10	Ser	Pro	Pro	His	Gly	Ser	Pro	Gly	Leu	Ala	Pro	Asn	Gln	Gln	Asn	Ile
	465					470					475					480
	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	Ser	Pro	Lys	Ile	Ala	Ser	His	Gln
15					485					490					495	
	Phe	Ser	Pro	Val	Ala	Gly	Val	His	Ser	Pro	Met	Ala	Ser	Ser	Gly	Asn
				500					505						510	
20	Thr	Gly	Asn	His	Ser	Phe	Ser	Ser	Ser	Ser	Leu	Ser	Ala	Leu	Gln	Ala
			515					520					525			
	Ile	Ser	Glu	Gly	Val	Gly	Thr	Ser	Leu	Leu	Ser	Thr	Leu	Ser	Ser	Pro
25			530				535					540				
	Gly	Pro	Lys	Leu	Asp	Asn	Ser	Pro	Asn	Met	Asn	Ile	Thr	Gln	Pro	Ser
	545					550					555					560
	Lys	Val	Ser	Asn	Gln	Asp	Ser	Lys	Ser	Pro	Leu	Gly	Phe	Tyr	Cys	Asp
30					565					570					575	
	Gln	Asn	Pro	Val	Glu	Ser	Ser	Met	Cys	Gln	Ser	Asn	Ser	Arg	Asp	His
				580					585					590		
35	Leu	Ser	Asp	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Val	Glu	Gly	Ala	Glu	Asn
			595					600					605			
	Gln	Arg	Gly	Pro	Leu	Glu	Ser	Lys	Gly	His	Lys	Lys	Leu	Leu	Gln	Leu
		610					615					620				
40	Leu	Thr	Cys	Ser	Ser	Asp	Asp	Arg	Gly	His	Ser	Ser	Leu	Thr	Asn	Ser
		625				630					635					640
	Pro	Leu	Asp	Ser	Ser	Cys	Lys	Glu	Ser	Ser	Val	Ser	Val	Thr	Ser	Pro
45					645					650					655	
	Ser	Gly	Val	Ser	Ser	Ser	Thr	Ser	Gly	Gly	Val	Ser	Ser	Thr	Ser	Asn
			660						665					670		
50	Met	His	Gly	Ser	Leu	Leu	Gln	Glu	Lys	His	Arg	Ile	Leu	His	Lys	Leu
			675					680					685			
	Leu	Gln	Asn	Gly	Asn	Ser	Pro	Ala	Glu	Val	Ala	Lys	Ile	Thr	Ala	Gln
		690					695					700				
55	Ala	Thr	Gly	Lys	Asp	Thr	Ser	Ser	Ile	Thr	Ser	Cys	Gly	Asp	Gly	Asn
	705					710					715					720

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SECRET-16574060

	Val	Val	Lys	Gln	Glu	Gln	Leu	Ser	Pro	Lys	Lys	Lys	Glu	Asn	Asn	Ala
					725					730						735
5	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Arg	Asp	Asp	Pro	Ser	Asp	Ala	Leu	Ser
				740					745					750		
	Lys	Glu	Leu	Gln	Pro	Gln	Val	Glu	Gly	Val	Asp	Asn	Lys	Met	Ser	Gln
			755					760					765			
10	Cys	Thr	Ser	Ser	Thr	Ile	Pro	Ser	Ser	Ser	Gln	Glu	Lys	Asp	Pro	Lys
		770					775					780				
	Ile	Lys	Thr	Glu	Thr	Ser	Glu	Glu	Gly	Ser	Gly	Asp	Leu	Asp	Asn	Leu
15	785					790					795					800
	Asp	Ala	Ile	Leu	Gly	Asp	Leu	Thr	Ser	Ser	Asp	Phe	Tyr	Asn	Asn	Ser
					805					810					815	
20	Ile	Ser	Ser	Asn	Gly	Ser	His	Leu	Gly	Thr	Lys	Gln	Gln	Val	Phe	Gln
				820					825					830		
	Gly	Thr	Asn	Ser	Leu	Gly	Leu	Lys	Ser	Ser	Gln	Ser	Val	Gln	Ser	Ile
25			835					840					845			
	Arg	Pro	Pro	Tyr	Asn	Arg	Ala	Val	Ser	Leu	Asp	Ser	Pro	Val	Ser	Val
		850					855					860				
	Gly	Ser	Ser	Pro	Pro	Val	Lys	Asn	Ile	Ser	Ala	Phe	Pro	Met	Leu	Pro
30	865					870					875				880	
	Lys	Gln	Pro	Met	Leu	Gly	Gly	Asn	Pro	Arg	Met	Met	Asp	Ser	Gln	Glu
					885					890					895	
35	Asn	Tyr	Gly	Ser	Ser	Met	Gly	Gly	Pro	Asn	Arg	Asn	Val	Thr	Val	Thr
				900					905					910		
	Gln	Thr	Pro	Ser	Ser	Gly	Asp	Trp	Gly	Leu	Pro	Asn	Ser	Lys	Ala	Gly
			915					920					925			
40	Arg	Met	Glu	Pro	Met	Asn	Ser	Asn	Ser	Met	Gly	Arg	Pro	Gly	Gly	Asp
		930					935					940				
	Tyr	Asn	Thr	Ser	Leu	Pro	Arg	Pro	Ala	Leu	Gly	Gly	Ser	Ile	Pro	Thr
45	945					950					955				960	
	Leu	Pro	Leu	Arg	Ser	Asn	Ser	Ile	Pro	Gly	Ala	Arg	Pro	Val	Leu	Gln
					965					970					975	
50	Gln	Gln	Gln	Gln	Met	Leu	Gln	Met	Arg	Pro	Gly	Glu	Ile	Pro	Met	Gly
				980					985					990		
	Met	Gly	Ala	Asn	Pro	Tyr	Gly	Gln	Ala	Ala	Ala	Ser	Asn	Gln	Leu	Gly
		995						1000					1005			
55	Ser	Trp	Pro	Asp	Gly	Met	Leu	Ser	Met	Glu	Gln	Val	Ser	His	Gly	Thr
	1010						1015					1020				

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	Gln Asn Arg Pro Leu Leu Arg Asn Ser Leu Asp Asp Leu Val Gly Pro	1025	1030	1035	1040
5	Pro Ser Asn Leu Glu Gly Gln Ser Asp Glu Arg Ala Leu Leu Asp Gln	1045		1050	1055
	Leu His Thr Leu Leu Ser Asn Thr Asp Ala Thr Gly Leu Glu Glu Ile	1060		1065	1070
10	Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Asn Gln Gly Gln Ala Leu	1075		1080	1085
	Glu Pro Lys Gln Asp Ala Phe Gln Gly Gln Glu Ala Ala Val Met Met	1090		1095	1100
15	Asp Gln Lys Ala Gly Leu Tyr Gly Gln Thr Tyr Pro Ala Gln Gly Pro	1105		1110	1115
	Pro Met Gln Gly Gly Phe His Leu Gln Gly Gln Ser Pro Ser Phe Asn	1125		1130	1135
20	Ser Met Met Asn Gln Met Asn Gln Gln Gly Asn Phe Pro Leu Gln Gly	1140		1145	1150
25	Met His Pro Arg Ala Asn Ile Met Arg Pro Arg Thr Asn Thr Pro Lys	1155		1160	1165
	Gln Leu Arg Met Gln Leu Gln Gln Arg Leu Gln Gly Gln Gln Phe Leu	1170		1175	1180
30	Asn Gln Ser Arg Gln Ala Leu Glu Leu Lys Met Glu Asn Pro Thr Ala	1185		1190	1195
	Gly Gly Ala Ala Val Met Arg Pro Met Met Gln Pro Gln Gln Gly Phe	1205		1210	1215
35	Leu Asn Ala Gln Met Val Ala Gln Arg Ser Arg Glu Leu Leu Ser His	1220		1225	1230
40	His Phe Arg Gln Gln Arg Val Ala Met Met Met Gln Gln Gln Gln Gln	1235		1240	1245
	Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	1250		1255	1260
45	Gln Gln Gln Thr Gln Ala Phe Ser Pro Pro Pro Asn Val Thr Ala Ser	1265		1270	1275
	Pro Ser Met Asp Gly Leu Leu Ala Gly Pro Thr Met Pro Gln Ala Pro	1285		1290	1295
50	Pro Gln Gln Phe Pro Tyr Gln Pro Asn Tyr Gly Met Gly Gln Gln Pro	1300		1305	1310
55	Asp Pro Ala Phe Gly Arg Val Ser Ser Pro Pro Asn Ala Met Met Ser	1315		1320	1325

Ser Arg Met Gly Pro Ser Gln Asn Pro Met Met Gln His Pro Gln Ala
1330 1335 1340

5 Ala Ser Ile Tyr Gln Ser Ser Glu Met Lys Gly Trp Pro Ser Gly Asn
1345 1350 1355 1360

Leu Ala Arg Asn Ser Ser Phe Ser Gln Gln Gln Phe Ala His Gln Gly
1365 1370 1375

10

Asn Pro Ala Val Tyr Ser Met Val His Met Asn Gly Ser Ser Gly His
1380 1385 1390

15

Met Gly Gln Met Asn Met Asn Pro Met Pro Met Ser Gly Met Pro Met
1395 1400 1405

Gly Pro Asp Gln Lys Tyr Cys *
1410 1415

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